AMENDMENTS TO THE SPECIFICATION

Please amend the specification at page 1 by replacing the paragraph starting at line 4 with the following paragraph:

This application claims priority from U.S. Provisional Application Serial No. 60/253,695, filed on November 20, 2000, and U.S. Provisional Application Serial No. 60/251,662, filed on December 6, 2000 and U.S. Utility Application Serial No. 09/988,842, filed on November 19, 2001 and issued as U.S. Patent No. 6,716,589.

Please replace the paragraph that starts at line 4 of page 6 with the following paragraph

FIG. 2 is a set of diagrams that depict the characteristics of long discordant helix segments. Amino acid sequences, together with determined and predicted secondary structure elements for sequences having ≥9=residue discordant segments are shown. Also shown are those discordant segments of Aβ, mouse PrP, and human PrP. The proteins are grouped by the length of their discordant stretch. The experimentally determined helical segments are drawn as ~~blue~~ grey cylinders in the bottom row of each case in which the amino acid sequences and residue positions in the PDB entries of the corresponding proteins are given (SEQ ID NO:4-23). The locations of the β-strands predicted by PHD are visualized by yellow strands in the middle row of each case, wherein the reliability index for each residue is shown. The Chou-Fasman-based predictions averaged for 6-residue segments are plotted above residue 3 in each segment and given in the top row of each case. E and e denote extended structures (i.e., β-strands) predicted with high and low probability, respectively, as in Chou and Fasman (1978, Adv. Enzymol. 47:45-148), and H and h represent predicted helical structures in an analogous manner.

Replace the paragraph starting at line 18 of page 6 with the following paragraph:

FIG. 3 is a diagram that depicts the amino acid sequence (bottom row SEQ ID NO:24) and predicted secondary structure by PHD and according to Chou-Fasman analysis for a polyleucine analogue of SP-C (lung surfactant protein C). The PHD predictions including reliability indices are given in the middle row and the Chou-Fasman data in the top row, but in

this case an α-helix is predicted by both methods, symbolized by a ~~blue~~ grey cylinder for the PHD prediction.

Replace the paragraph starting at line 27 of page 6 with the following paragraph:

FIG. 5 is a set of diagrams that depict the experimentally determined and predicted secondary structures of positions 1-28 of Aβ (SEQ ID NO:25). and a variant of Aβ (1-28) in which three residues have been changed to alanine (K16A, L17A, F20A, SEQ ID NO:26)). Symbols are as described for FIGS. 2 and 4.

Replace the paragraph starting at line 12 of page 7 with the following three paragraphs:

FIG. 10A depicts the KAD peptide in an energy-minimized conformation ~~(top structure), the KAD peptide in an extended conformation (middle structure), and the KFFE (SEQ ID NO: 1) peptide in an extended conformation (bottom structure).~~ The amino and carboxyl groups of the charged side-chains are on the same side of the polypeptide backbone in KAD and the distances between them are then shown. ~~In KFFE, the charged side-chains are on opposite sides of the polypeptide backbone.~~

FIG. 10B depicts the KAD peptide in an extended conformation. The amino and carboxyl groups of the charged side-chains are on the same side of the polypeptide backbone in KAD and the distances between them are then shown.

FIG. 10C depicts the KFFE (SEQ ID NO:1) peptide in an extended conformation. In KFFE, the charged side-chains are on opposite sides of the polypeptide backbone.

Replace the paragraph starting at line 18 of page 7 with the following two paragraphs:

FIG. 11A depicts the charge separation of Aβ(15-23) in α-helical and β-strand conformations. The ~~upper panel shows the~~ Aβ(15-23) region is in helical conformation, symbolized by the cylinder. The charged side-chains Lys16, Glu22 and Asp23 are shown. ~~In the lower panel, the A.beta.(15-23) region is modeled in .beta. strand/extended conformation, indicated by the wavy strand.~~ The charged side-chains are shown. For the helical conformation, the distances between the ε-amino group of Lys16 and the γ-carboxyl group of Glu22 and the β-

carboxyl group of Asp23 are shown, and for the extended conformation the Lys16-Glu22 distance is indicated.

FIG. 11B depicts the charge separation of Aβ(15-23) in α-helical and β-strand conformations. The Aβ(15-23) region is modeled in β-strand/extended conformation, indicated by the wavy strand. The charged side-chains are shown. For the helical conformation, the distances between the ε-amino group of Lys16 and the γ-carboxyl group of Glu22 and the β-carboxyl group of Asp23 are shown, and for the extended conformation the Lys16-Glu22 distance is indicated.